

Serial Number: 09/165,460

CRF Processing Date: 8/15/2000
Entered by: [Signature]
Verified by: [Signature] (STIC sta

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically:
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included:
- ☐ Deleted extra, invalid, headings used by an applicant, specifically:
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically:
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Sequence 4 - moved (ix) FEATURE: and (ii) MOLECULE TYPE:
section above (xi) SEQ DESCRIPT heading

AUG 21 2000

TECH CENTER 1000/2500

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

P. Tung

1652

RAW SEQUENCE LISTING DATE: 08/15/2000
PATENT APPLICATION: US/09/165,460 TIME: 15:32:18

Input Set : A:\Sequence
Output Set: N:\CRF3\08152000\I165460.raw

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

C--> 4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: Rine, Jasper D.
7 Boyartchuk, Victor L.
8 Ashby, Matthew N.
C--> 10 (ii) TITLE OF INVENTION: AFC1 AND RCE1: ISOPRENYLATED CAAX
11 PROCESSING ENZYMES
13 (iii) NUMBER OF SEQUENCES: 4
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Fish & Richardson P.C.
17 (B) STREET: 2200 Sand Hill road, suite 100
18 (C) CITY: Menlo Park
19 (D) STATE: CA
20 (E) COUNTRY: USA
21 (F) ZIP: 94025
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Diskette
25 (B) COMPUTER: IBM Compatible
26 (C) OPERATING SYSTEM: DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
29 (vi) CURRENT APPLICATION DATA:
C--> 30 (A) APPLICATION NUMBER: US/09/165,460
C--> 31 (B) FILING DATE: 02-Oct-1998
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: 08/902,774
35 (B) FILING DATE: 30-JUL-1997
37 (A) APPLICATION NUMBER: 60/023,491
38 (B) FILING DATE: 07-AUG-1996
40 (viii) ATTORNEY/AGENT INFORMATION:
41 (A) NAME: Suyat, Reginald J.
42 (B) REGISTRATION NUMBER: 28,172
43 (C) REFERENCE/DOCKET NUMBER: 09272-006004
45 (ix) TELECOMMUNICATION INFORMATION:
46 (A) TELEPHONE: 650/322-5070
47 (B) TELEFAX: 650/854-0875

ERRORED SEQUENCES

231 (2) INFORMATION FOR SEQ ID NO: 4:
233 (i) SEQUENCE CHARACTERISTICS:
234 (A) LENGTH: 315 amino acids
235 (B) TYPE: amino acid
236 (D) TOPOLOGY: unknown
238 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
E--> 240 (ii) MOLECULE TYPE: peptide
E--> 242 (ix) FEATURES:

RAW SEQUENCE LISTING DATE: 08/15/2000
 PATENT APPLICATION: US/09/165,460 TIME: 15:32:18

Input Set : A:\Sequence
 Output Set: N:\CRF3\08152000\I165460.raw

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E--> 243      (A) NAME/KEY: peptide
      244      (B) LOCATION: 1...315
E--> 245      (D) OTHER INFORMATION: /note = "The sequence of the Rcelp
E--> 246      protein from yeast presented as a polypeptide sequence"
E--> 248  Met Leu Gln Phe Ser Thr Phe Leu Val Leu Leu Tyr Ile Ser Ile Ser
      249      1          5          10          15
      250  Tyr Val Leu Pro Leu Tyr Ala Thr Ser Gln Pro Glu Gln Ser Lys Arg
      251      20          25          30
      252  Asp Asn Pro Arg Thr Ile Lys Ser Arg Met Gln Lys Leu Thr Ile Met
      253      35          40          45
      254  Leu Ile Ser Asn Leu Phe Leu Val Pro Phe Leu Gln Ser Gln Leu Ser
      255      50          55          60
      256  Ser Thr Thr Ser His Ile Gly Phe Lys Asp Ala Phe Leu Gly Leu Gly
      257      65          70          75          80
      258  Ile Ile Pro Gly Tyr Tyr Ala Ala Leu Pro Asn Pro Trp Gln Phe Ser
      259      85          90          95
      260  Gln Phe Val Lys Asp Leu Thr Lys Cys Val Ala Met Leu Leu Thr Leu
      261      100         105         110
      262  Tyr Cys Gly Pro Val Leu Asp Phe Val Leu Tyr His Leu Leu Asn Pro
      263      115         120         125
      264  Lys Ser Ser Ile Leu Glu Asp Phe Tyr His Glu Phe Leu Asn Ile Trp
      265      130         135         140
      266  Ser Phe Arg Asn Phe Ile Phe Ala Pro Ile Thr Glu Glu Ile Phe Tyr
      267      145         150         155         160
      268  Thr Ser Met Leu Leu Thr Thr Tyr Leu Asn Leu Ile Pro His Ser Gln
      269      165         170         175
      270  Leu Ser Tyr Gln Gln Leu Phe Trp Gln Pro Ser Leu Phe Phe Gly Leu
      271      180         185         190
      272  Ala His Ala His His Ala Tyr Glu Glu Leu Gln Glu Gly Ser Met Thr
      273      195         200         205
      274  Thr Val Ser Ile Leu Leu Thr Thr Cys Phe Gln Ile Leu Tyr Thr Thr
      275      210         215         220
      276  Leu Phe Gly Gly Leu Thr Lys Phe Val Phe Val Arg Thr Gly Gly Asn
      277      225         230         235         240
      278  Leu Trp Cys Cys Ile Ile Leu His Ala Leu Cys Asn Ile Met Gly Phe
      279      245         250         255
      280  Pro Gly Pro Ser Phe Leu Asn Leu His Phe Thr Val Val Asp Lys Lys
      281      260         265         270
      282  Ala Gly Arg Ile Ser Lys Leu Val Ser Ile Trp Asn Lys Cys Tyr Phe
      283      275         280         285
      284  Ala Leu Leu Val Leu Gly Leu Ile Ser Leu Lys Asp Thr Leu Gly Thr
      285      290         295         300
      286  Leu Val Gly Thr Pro Gly Tyr Arg Ile Thr Leu
E--> 287  305          310          315
  
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VERIFICATION SUMMARY DATE: 08/15/2000
 PATENT APPLICATION: US/09/165,460 TIME: 15:32:19

Input Set : A:\Sequence
 Output Set: N:\CRF3\08152000\I165460.raw

L:4 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
 L:10 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
 L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
 L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
 L:164 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
 L:240 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:240 M:330 E: (2) Invalid Amino Acid Designator, 4
 L:242 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
 L:242 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:242 M:330 E: (2) Invalid Amino Acid Designator, 2
 M:332 Repeated in SeqNo=4
 L:243 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:243 M:330 E: (2) Invalid Amino Acid Designator, 3
 L:245 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:245 M:330 E: (2) Invalid Amino Acid Designator, 10
 L:246 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:246 M:330 E: (2) Invalid Amino Acid Designator, 7
 L:287 M:203 E: No. of Seq. differs, LENGTH:Input:315 Found:342 SEQ:4
 L:245 M:202 E: (16) Value must be an Integer, Data=[/note = "The sequence of the Rcelp]
 L:262 M:220 C: Keyword misspelled or invalid format, Poss data loss, Seq -1, (D) OTHER INFORMATION:
 L:278 M:220 C: Keyword misspelled or invalid format, Poss data loss, Seq -1, (D) OTHER INFORMATION:

RAW SEQUENCE LISTING DATE: 08/17/2000
 PATENT APPLICATION: US/09/165,460 TIME: 20:12:25

Input Set : A:\Pto.amc
 Output Set: N:\CRF3\08172000\I165460.raw

AUG 21 2000

TECH CENTER 1000/2000

SEQUENCE LISTING

C--> 4 (1) GENERAL INFORMATION:
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 7 Boyartchuk, Victor L.
 8 Ashby, Matthew N.
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 11 PROCESSING ENZYMES
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 16 (A) ADDRESSEE: Fish & Richardson P.C.
 17 (B) STREET: 2200 Sand Hill road, suite 100
 18 (C) CITY: Menlo Park
 19 (D) STATE: CA
 20 (E) COUNTRY: USA
 21 (F) ZIP: 94025
 23 (v) COMPUTER READABLE FORM:
 24 (A) MEDIUM TYPE: Diskette
 25 (B) COMPUTER: IBM Compatible
 26 (C) OPERATING SYSTEM: DOS
 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
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 33 (vii) PRIOR APPLICATION DATA:
 34 (A) APPLICATION NUMBER: 08/902,774
 35 (B) FILING DATE: 30-JUL-1997
 37 (A) APPLICATION NUMBER: 60/023,491
 38 (B) FILING DATE: 07-AUG-1996
 40 (viii) ATTORNEY/AGENT INFORMATION:
 41 (A) NAME: Suyat, Reginald J.
 42 (B) REGISTRATION NUMBER: 28,172
 43 (C) REFERENCE/DOCKET NUMBER: 09272-006004
 45 (ix) TELECOMMUNICATION INFORMATION:
 46 (A) TELEPHONE: 650/322-5070
 47 (B) TELEFAX: 650/854-0875
 50 (2) INFORMATION FOR SEQ ID NO: 1:
 52 (i) SEQUENCE CHARACTERISTICS:
 53 (A) LENGTH: 1825 base pairs
 54 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: unknown
 56 (D) TOPOLOGY: unknown
 58 (ii) MOLECULE TYPE: Genomic DNA
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 62 ACCTACCTTT TTTTCTATCT TCAACAACGA AACGCCTTAC ACACACACAC ACATACATCT 60
 63 ACATACATAC ATACAAATAT ACATATATGT AAACCTTGAT ATTCATTCCT ATTAACCAAA 120
 64 AAGAGGCAAT TAAACTTTTC CCTCTTTTTC TACGTCATT ACTCAAAAAC TCTAATTCCT 180
 65 TCGTCTCTGT TCTGCCATTT TCTCCAGAAA AAAATCGACG GGAAATAAAA AAAAAAAGAC 240

RAW SEQUENCE LISTING DATE: 08/17/2000
 PATENT APPLICATION: US/09/165,460 TIME: 20:12:25

Input Set : A:\Pto.amc
 Output Set: N:\CRF3\08172000\I165460.raw

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66 AACGAACAAG AGAAAAAGTT CGCGAATTAT AAACCACTTC TATAATTAAC AGGAAAAGGA 300
67 AGGAAAAAAA AGGAGGAAAA GAAACCTGCA GGCCTTTTATT CATGTTTGAT CTTAAGACGA 360
68 TTCTCGACCA TCCTAATATC CCGTGGAAAT TAATCATTTC TGGGTTCTCG ATTGCCCAAT 420
69 TTTCTTTTCA ATCTTACTTG ACGTACAGAC AGTACCAGAA GCTATCTGAA ACAAAGTTGC 480
70 CACCTGTGCT GGAAGACGAA ATTGATGATG AAACCTTTCA TAAATCAAGG AACTACTCCC 540
71 GGGCCAAGGC CAAGTTCTCC ATTTTCGGTG ACGTCTATAA CCTAGCCCAA AAGCTAGTTT 600
72 TCATCAAATA CGACCTCTTC CCTAAAATCT GGCACATGGC CGTTTCTTTA TTGAATGCAG 660
73 TCCTGCCAGT CAGATTTTCT ATGGTCTCCA CTGTCCGACA GAGTTTATAG CTTCTTGGGT 720
74 CTCTTATCCA GTTTGCTTAC CTTGGTTGAT TTGCCACTCT CTTACTATAG CCATTTTGTC 780
75 CTGGAAGAAA AATTTGGTTT CAATAAATTG ACCGTCCAAC TATGGATCAC CGATATGATC 840
76 AAGAGTCTGA CTTTGGCGTA TGCTATTGGT GGCCCAATCC TTTACCTGTT CCTTAAGATC 900
77 TTTGATAAAT TCCCTACTGA TTTCTTTGGG TACATTATGG TCTTCTTGTT CGTTGTCCAA 960
78 ATCTTAGCCA TGACAATCAT TCCAGTCTTC ATCATGCCCA TGTTTAATAA GTTCACTCCA 1020
79 TTGGAGGAGC GTGAAGTCAA AAAATCTATT GAAAGTTTGG CCGATAGAGT TGGGTTCCCT 1080
80 CTAGATAAGA TTTTGTCTAT TGACGGCTCA AAAAGATCTT CTCATTCAA CGCATATTTT 1140
81 ACAGGTTTGC CATTCACCTC CAAGAGAATT GTTTGTTCG ACACTTTAGT GAACAGTAAT 1200
82 TCTACTGATG AAATTACGGC TGTTTTGGCC CATGAAATCG GTCACCTGGC AAAAAACCAC 1260
83 ATCGTTAATA TGGTCATCTT TAGTCAATTG CACACCTTCC TCATTTTCTC CTTTTCACC 1320
84 AGCATCTACA GAAATACATC ATTTTACAAC ACCCTCGGCT TTTTCTTAGA GAAGTCCACT 1380
85 GGCAGTTTGG TTGATCCCGT TATCACAAGG GAATTCCTCA TTATCATTGG ATTTATGTTA 1440
86 TTTAAGCACT TATTAACCTC ACTCGAATGT GCCATGCAAT TCGTGATGAG TTTAATTTCC 1500
87 AGAAGTCTAG AATATCAAGC TGATGCTTAT GCTAAAAAAT TGGGCTACAA GCAAAATCTA 1560
88 TGTAGGGCTC TAATTGATCT ACAAATCAAA AACCTTTCCA CCATGAATGT AGATCCTCTG 1620
89 TATTCTAGCT ATCATTTATC CCATCCAACCT CTAGCTGAAA GATCGACCGC TCTAGACTAT 1680
90 GTTAGTGAAA AGAAGAAAAA CTAATCTATA GAGTACACAT ATTAGCATGT ACCGTTAAAT 1740
91 TCAGCTTCGT TATGCTCTATA TCTACATACA TACACAGGTA TCTACTATAA GAATAAAGGA 1800
92 AAGAAAAAAT AAACGATTAA ACATT 1825
94 (2) INFORMATION FOR SEQ ID NO: 2:
96 (i) SEQUENCE CHARACTERISTICS:
97 (A) LENGTH: 2850 base pairs
98 (B) TYPE: nucleic acid
99 (C) STRANDEDNESS: unknown
100 (D) TOPOLOGY: unknown
102 (ii) MOLECULE TYPE: Genomic DNA
104 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
106 TGAAGTGTG ATGAACAAAG AGAAGCTGAC AAGCATCAAA GCTTGTACG ATGATTTCCA 60
107 TTCAAAAAAT TGTGAATATG AAACCAAGTT CAACAAGAAT TTTCTTGAAT TAAATGAGTT 120
108 ATATAATATG AATAGGGGAG ACCGTAGGCC AAAGGAAGT AAATTTACAG ATTTTATTAC 180
109 TTCACAGCTG TTTAACGATA TCGAAAGCAT TTGCAACTTG AAAGTTAGTG TTCACAACCT 240
110 ATCCAACATT TTTAAAAAAC AGGTCAGTAC CCTAAAACAA CACTCAAAGC ACGCATTATC 300
111 TGAGGATTCA ATATCGCACA CAGGTAACGG TAGTTCATCG TCGCCAGTT CAGCGTCATT 360
112 AACGCCAGTA ACTTCTTCAT CCAAGAGTAG TTTATTTTTA CCTAGCGGTA GCTCGTCTAC 420
113 TTCCCTGAAA TTTACAGACC AGATTGTTCA TAAATGGGTT AGGATTGCTC CTTTACAGTA 480
114 CAAACGAGAC ATTAATGTGA ACTTGAATT TAATAAGGAC ATTAAGGAAA CTTTAATTCC 540
115 AAGTTTGTAA AGCTGCCTAT GTTGTAGGTT TTATTGCGTT CGAGTAATGA TTAATTTTGA 600
116 AAACCATCTT GGCGTAGCGA AGATTGATAT CCTATTCTT GTTAGGCAAG TGACAAAATA 660
117 AAAAAACATT AGAAAAAATT CTCGTTACTT TTCTTATAGA TATAGATATA TGTATGGTTT 720
118 GCTTATAGAT GAAGGTATTT ATCGCGTCCT TTGTATTTCC TATTATTAAT AAAATTCTTT 780
119 TAAATGCAT TTCTGGTGC TCTTTTGTG CTTCTGTATT TTTTTTTTTT TGGACCACTG 840

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RAW SEQUENCE LISTING DATE: 08/17/2000
 PATENT APPLICATION: US/09/165,460 TIME: 20:12:25

Input Set : A:\Pto.amc
 Output Set: N:\CRF3\08172000\I165460.raw

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120 GATGGAACAC CTTTGATGAT TTTATTACCT TTATTTTAAC TTAATAAAAT ATCGAGATTT 900
121 CAGGAACAAA ACATAGAATT TTCTTTGTCA AGAAAAATAA AACGAAATAA ATTGATGCTT 960
122 TGACTACTGA CTGTCTGTCA TAGAGAGAAC CAGAACAGCA ATGCTACAAT TCTCAACATT 1020
123 TCTAGTGTCT CTATACATCT CCATATCCTA TGTGCTACCG CTATATGCAA CTTCAACAACC 1080
124 AGAAGGGTCT AAACGAGATA ATCCTCGAAC GATTAAATCT CGCATGCAAA AACTTACAAT 1140
125 TATGCTAATT TCCAACCTTT TTTTGGTGCC TTTTTCACAA TCTCAATTAT CTAGTACCAC 1200
126 TTCACATATA AGTTTCAAGG ACGCATTTTT AGGCTTAGGT ATTATCCCAG GTTATTACGC 1260
127 TGCATTGCCA AACCTTGGC AATTCAGCCA GTTCGTGAAA GACTTAACGA AATGTGTTC 1320
128 GATGTTATTG ACCTTATATT GTGGACCCGT TTTAGATTTT GTATTATATC ATTTATTAAA 1380
129 TCCAAAGAGC TCTATACTTG AAGATTTTTC CCATGAATTC CTGAATATTT GGAGTTTCAG 1440
130 GAATTTTATA TTTGACACCA TAACTGAGGA AATATTTTAC ACGTCAATGC TTTTGACTAC 1500
131 GACTTAAAC CTAATACCGC ATTCGCAACT AAGCTATCAA CAGTTATTTT GGCAACCATC 1560
132 ACCGTTTTTT GGACTTGGC ACGCACACCA TGCTTAGGAG CAATTACAGG AAGGCTCCAT 1620
133 GACAACTGTT TCCATTCTGC TGACAACATG CTTCCAAATT TTATACACAA CACTTTTGG 1680
134 AGGGTTAACC AAGTTTGTAT TGCAATATCA TGGGGTTTAA TGGTCCTTCA AGATTGAATT 1740
135 TACATTTTCA AGTAGTAGAC AAGAAAGCTG GACGCATTTC CAAATTGGTC TCTCAATCTG 1800
136 GAATAAGTGC TACTTCGCAC TGCTGGTCCT TGGATTAATA TCCCTGAAGG ATACCTTACA 1860
137 AACTCTGGTA GGAACCTCTG GTTATAGAAT AACCCTTTAG CCTTTTTTAC GACTTGTAT 1920
138 ACCGTTTTAA ATTTCTATG TACTATAACC TTTTTCACCT ACTATTATGG AATTCTATCG 1980
139 AGCGACCGGG CTTTGTGTAC GGAAGAGTGA AAAAATCGAG TTTTGGTGTT TTGGTGAAAG 2040
140 AATTTGGAGG ACTATAAAGT ACCTATACTT TGTATTACGG ACTCAATAAC AAGTCGTTCC 2100
141 TGTCAGTGGT ATTGAAGTTG TCAGATCTAA GAGTAGAGAG AAGGTGGCAT CTAATAGGTT 2160
142 TCGACGTTTT TCTTTTTTTA AGGTTTTTAT TTGCTCTCCT AGAATTTAAG GTCTTAGTTA 2220
143 GTTTTGGTTT GTTTTGTGGG TTACATATTT TCAATTCAAA GGAGAATTTA GCTGTCTTTT 2280
144 ATAATGTCCA ATAGAGATAA CGAGAGCATG CTGCGTACTA CATCAAGCGA TAAGGCGATC 2340
145 GCTAGTCAAA GGGATAAACG GAAGTCTGAA GTTTTGATTG CTGCACAGTC CCTTGACAAT 2400
146 GAAATCCGCA GCGTAAAAAA CCTAAAAAGA TTGTCGATTG GGTCAATGGA TTTACTTATT 2460
147 GATCCAGAAT TAGATATAAA ATTCGGTGGG GAATCTAGTG GGAGACGATC ATGGTCTGGC 2520
148 ACGACATCCA GTTCGCGTC AATGCCAAGT GACACAACCA CCGTTAATAA CACACGATAT 2580
149 AGCGATCCAA CTCCGCTAGA GAACCTGCAT GGGAGGGGTA ACTCAGGGAT AGAATCCTCC 2640
150 AATAAGACTA AAATTAAATG CTAACGTATT AAAGAAAAAC TTATTATGGG TTCCCGCCAA 2700
151 TCAACACCCCT AACGTTAAGC CTGATAATTT CCTAGAGCTT GTACAAGATA CTTTACAAAA 2760
152 TATCAACTA AGCGACAATG GTGAAGATAA TGATGGGAAT AGCAATGAAA ATAACGATAT 2820
153 TGAGGATAAT GGGGAGGATA AAGAATCACA 2850

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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

158 (A) LENGTH: 451 amino acids
 159 (B) TYPE: amino acid
 160 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

C--> 164 (ix) FEATURE:

165 (A) NAME/KEY: peptide
 166 (B) LOCATION: 1..451
 167 (D) OTHER INFORMATION: /note = "The sequence of the Afc1p
 168 protein from yeast presented as a polypeptide sequence"

170 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

172 Met Phe Asp Leu Lys Thr Ile Leu Asp His Pro Asn Thr Pro Trp Lys
 173 1 5 10 15
 174 Leu Ile Ile Ser Gly Phe Ser Ile Ala Gln Phe Ser Phe Glu Ser Tyr

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/165,460
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Input Set : A:\Pto.amc
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175          20          25          30
176 Leu Thr Tyr Arg Gln Tyr Gln Lys Leu Ser Glu Thr Lys Leu Pro Pro
177          35          40          45
178 Val Leu Glu Asp Glu Ile Asp Asp Glu Thr Phe His Lys Ser Arg Asn
179          50          55          60
180 Tyr Ser Arg Ala Lys Ala Lys Phe Ser Ile Phe Gly Asp Val Tyr Asn
181          65          70          75          80
182 Leu Ala Gln Lys Leu Val Phe Ile Lys Tyr Asp Leu Phe Pro Lys Ile
183          85          90          95
184 Trp His Met Ala Val Ser Leu Leu Asn Ala Val Leu Pro Val Arg Phe
185          100          105          110
186 His Met Val Ser Thr Val Ala Gln Ser Leu Cys Phe Leu Gly Leu Leu
187          115          120          125
188 Ser Ser Leu Ser Thr Leu Val Asp Leu Pro Leu Ser Tyr Tyr Ser His
189          130          135          140
190 Phe Val Leu Glu Glu Lys Phe Gly Phe Asn Lys Leu Thr Val Gln Leu
191          145          150          155          160
192 Trp Ile Thr Asp Met Ile Lys Ser Leu Thr Leu Ala Tyr Ala Ile Gly
193          165          170          175
194 Gly Pro Ile Leu Tyr Leu Phe Leu Lys Ile Phe Asp Lys Phe Pro Thr
195          180          185          190
196 Asp Phe Leu Trp Tyr Ile Met Val Phe Leu Phe Val Val Gln Ile Leu
197          195          200          205
198 Ala Met Thr Ile Ile Pro Val Phe Ile Met Pro Met Phe Met Lys Phe
199          210          215          220
200 Thr Pro Leu Glu Asp Gly Glu Leu Lys Lys Ser Ile Glu Ser Leu Ala
201          225          230          235          240
202 Asp Arg Val Gly Phe Pro Leu Asp Lys Ile Phe Val Ile Asp Gly Ser
203          245          250          255
204 Lys Arg Ser Ser His Ser Asn Ala Tyr Phe Thr Gly Leu Pro Phe Thr
205          260          265          270
206 Ser Lys Arg Ile Val Leu Phe Asp Thr Leu Val Asn Ser Asn Ser Thr
207          275          280          285
208 Asp Glu Ile Thr Ala Val Leu Ala His Glu Ile Gly His Trp Gln Lys
209          290          295          300
210 Met His Ile Val Asn Met Val Ile Phe Ser Gln Leu His Thr Phe Leu
211          305          310          315          320
212 Ile Phe Ser Leu Phe Thr Ser Ile Tyr Arg Asn Thr Ser Phe Tyr Asn
213          325          330          335
214 Thr Phe Gly Phe Phe Leu Glu Lys Ser Thr Gly Ser Ser Phe Val Asp
215          340          345          350
216 Pro Val Ile Thr Lys Glu Phe Pro Ile Ile Ile Gly Phe Met Leu Phe
217          355          360          365
218 Asn Asp Leu Leu Thr Pro Leu Glu Cys Ala Met Gln Phe Val Met Ser
219          370          375          380
220 Leu Ile Ser Arg Thr His Glu Tyr Gln Ala Asp Ala Tyr Ala Lys Lys
221          385          390          395          400
222 Leu Gly Tyr Lys Gln Asn Leu Cys Arg Ala Leu Ile Asp Leu Gln Ile
223          405          410          415

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224 Lys Asn Leu Ser Thr Met Asn Val Asp Pro Leu Tyr Ser Ser Tyr His
225                               420          425          430
226 Tyr Ser His Pro Thr Leu Ala Glu Arg Leu Thr Ala Leu Asp Tyr Val
227                               435          440          445
228 Ser Glu Lys
229                               450
231 (2) INFORMATION FOR SEQ ID NO: 4:
232 (i) SEQUENCE CHARACTERISTICS:
233 (A) LENGTH: 315 amino acids
234 (B) TYPE: amino acid
235 (D) TOPOLOGY: unknown
236 (ii) MOLECULE TYPE: peptide
237 (ix) FEATURE:
238 (A) NAME/KEY: peptide
239 (B) LOCATION: 1...315
240 (D) OTHER INFORMATION: /note = "The sequence of the Rcelp
241 protein from yeast presented as a polypeptide sequence"
242 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
243 Met Leu Gln Phe Ser Thr Phe Leu Val Leu Leu Tyr Ile Ser Ile Ser
244 1 5 10 15
245 Tyr Val Leu Pro Leu Tyr Ala Thr Ser Gln Pro Glu Gln Ser Lys Arg
246 20 25 30
247 Asp Asn Pro Arg Thr Ile Lys Ser Arg Met Gln Lys Leu Thr Ile Met
248 35 40 45
249 Leu Ile Ser Asn Leu Phe Leu Val Pro Phe Leu Gln Ser Gln Leu Ser
250 50 55 60
251 Ser Thr Thr Ser His Ile Gly Phe Lys Asp Ala Phe Leu Gly Leu Gly
252 65 70 75 80
253 Ile Ile Pro Gly Tyr Tyr Ala Ala Leu Pro Asn Pro Trp Gln Phe Ser
254 85 90 95
255 Gln Phe Val Lys Asp Leu Thr Lys Cys Val Ala Met Leu Leu Thr Leu
256 100 105 110
257 Tyr Cys Gly Pro Val Leu Asp Phe Val Leu Tyr His Leu Leu Asn Pro
258 115 120 125
259 Lys Ser Ser Ile Leu Glu Asp Phe Tyr His Glu Phe Leu Asn Ile Trp
260 130 135 140
261 Ser Phe Arg Asn Phe Ile Phe Ala Pro Ile Thr Glu Glu Ile Phe Tyr
262 145 150 155 160
263 Thr Ser Met Leu Leu Thr Thr Tyr Leu Asn Leu Ile Pro His Ser Gln
264 165 170 175
265 Leu Ser Tyr Gln Gln Leu Phe Trp Gln Pro Ser Leu Phe Phe Gly Leu
266 180 185 190
267 Ala His Ala His His Ala Tyr Glu Glu Leu Gln Glu Gly Ser Met Thr
268 195 200 205
269 Thr Val Ser Ile Leu Leu Thr Thr Cys Phe Gln Ile Leu Tyr Thr Thr
270 210 215 220
271 Leu Phe Gly Gly Leu Thr Lys Phe Val Phe Val Arg Thr Gly Gly Asn
272 225 230 235 240
273 Leu Trp Cys Cys Ile Ile Leu His Ala Leu Cys Asn Ile Met Gly Phe

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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/165,460 DATE: 08/17/2000
TIME: 20:12:26

Input Set : A:\Pto.amc
Output Set: N:\CRF3\08172000\I165460.raw

L:4 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:10 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:164 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]